

**AMENDMENTS TO SPECIFICATION**

**Replace the paragraph at page 1, lines 3-6, with the following:**

This application is a continuation-in-part claims the benefit of U.S.  
Application No. 09/291,922, filed April 14, 1999, now granted as U.S. Patent No.  
6,383,776, which claims priority to U.S. Provisional Application No. 60/083,044, filed  
April 24, 1998, the entire contents of which are hereby incorporated by reference.

**Replace the paragraph at page 2, lines 29-33, with the following:**

Figures 1A, 1B, 1C, 1D, 1E, 1F and 1G show Figure 1 shows a  
comparison of the amino acid sequences set forth in SEQ ID NOs:2, 4, 6, 8, 10, 12, 14,  
16, and 32 with the *Arabidopsis thaliana*-like sugar transport protein amino acid  
sequence set forth in SEQ ID NOs:29 and 37. Amino acid designations in small case  
letters represent regions that are thought to be *Arabidopsis thaliana*-like sugar transport  
protein signatures.

**Replace the paragraph at page 2, lines 34-36, with the following:**

Figures 2A, 2B, 2C and 2D show Figure 2 shows a comparison of the  
amino acid sequences set forth in SEQ ID NOs:18, 20, 22, 24, 26, 28, and 36 with the  
*Beta vulgaris*-like sugar transport protein amino acid sequence set forth in SEQ ID  
NO:30 and 38.

**Replace the paragraph at page 26, lines 9-16, with the following:**

Figures 1A, 1B, 1C, 1D, 1E, 1F and 1G present Figure 1 presents an  
alignment of the amino acid sequences set forth in SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14,  
16, and 32, and the *Arabidopsis* and rice sequences (SEQ ID NOs:29 and 37). The  
data in Table 5 represents a calculation of the percent identity of the amino acid

sequences set forth in SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, and 32, and the *Arabidopsis* and rice sequences (SEQ ID NOs:29 and 37). The BLAST pLog score for the corn sequence is the highest possible under the new BLAST format (i.e. >180.00), under the previous search (Table 3) this score would have been >250.00.

**Replace the paragraph at page 29, lines 14-21, with the following:**

Figures 2A, 2B, 2C and 2D present ~~Figure 2 presents~~ an alignment of the amino acid sequences set forth in SEQ ID NOs:18, 20, 22, 24, 26, 28, and 36, and the *Beta vulgaris* and rice sequences (SEQ ID NOs:30 and 38). The data in Table 5 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:18, 20, 22, 24, 26, 28, and 36, and the *Beta vulgaris* and rice sequences (SEQ ID NOs:30, and 38). The BLAST pLog score for the corn sequence is the highest possible under the new BLAST format (i.e. >180.00), under the previous search (Table 3) this score would have been >250.00.